



wwPDB EM Validation Summary Report ⓘ

Nov 16, 2022 – 04:58 PM EST

PDB ID : 7L70
EMDB ID : EMD-23209
Title : The eukaryotic translation initiation factor 2B from Homo sapiens in its apo form
Authors : Wang, L.; Schoof, M.; Lawrence, R.; Boone, M.; Frost, A.; Walter, P.
Deposited on : 2020-12-24
Resolution : 2.80 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

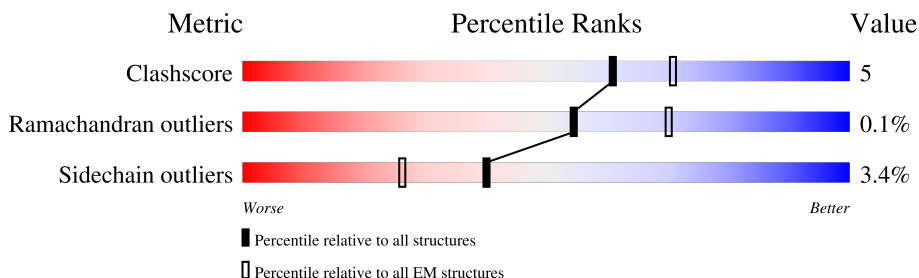
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	721	49% 7% 43%
1	B	721	48% 8% 43%
2	C	368	79% 7% 14%
2	D	368	77% 9% 14%
3	E	523	62% 6% 33%
3	F	523	60% 6% 34%
4	G	322	70% 10% 18%
4	H	322	73% 8% 17%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	I	452	<div><div><div>6%</div><div>42%</div><div>5%</div><div>52%</div></div></div>
5	J	452	<div><div><div>44%</div><div>6%</div><div>49%</div></div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24187 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Translation initiation factor eIF-2B subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	414	Total	C	N	O	S	0	0
			3195	2023	568	589	15		
1	B	414	Total	C	N	O	S	0	0
			3195	2023	568	589	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	587	VAL	ILE	conflict	UNP Q13144
B	587	VAL	ILE	conflict	UNP Q13144

- Molecule 2 is a protein called Translation initiation factor eIF-2B subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	318	Total	C	N	O	S	0	0
			2479	1568	438	458	15		
2	D	318	Total	C	N	O	S	0	0
			2472	1565	437	455	15		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	MET	-	initiating methionine	UNP P49770
C	-15	HIS	-	expression tag	UNP P49770
C	-14	HIS	-	expression tag	UNP P49770
C	-13	HIS	-	expression tag	UNP P49770
C	-12	HIS	-	expression tag	UNP P49770
C	-11	HIS	-	expression tag	UNP P49770
C	-10	HIS	-	expression tag	UNP P49770
C	-9	GLY	-	expression tag	UNP P49770
C	-8	GLY	-	expression tag	UNP P49770
C	-7	GLY	-	expression tag	UNP P49770
C	-6	SER	-	expression tag	UNP P49770

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	GLU	-	expression tag	UNP P49770
C	-4	ASN	-	expression tag	UNP P49770
C	-3	LEU	-	expression tag	UNP P49770
C	-2	TYR	-	expression tag	UNP P49770
C	-1	PHE	-	expression tag	UNP P49770
C	0	GLN	-	expression tag	UNP P49770
C	1	SER	-	expression tag	UNP P49770
D	-16	MET	-	initiating methionine	UNP P49770
D	-15	HIS	-	expression tag	UNP P49770
D	-14	HIS	-	expression tag	UNP P49770
D	-13	HIS	-	expression tag	UNP P49770
D	-12	HIS	-	expression tag	UNP P49770
D	-11	HIS	-	expression tag	UNP P49770
D	-10	HIS	-	expression tag	UNP P49770
D	-9	GLY	-	expression tag	UNP P49770
D	-8	GLY	-	expression tag	UNP P49770
D	-7	GLY	-	expression tag	UNP P49770
D	-6	SER	-	expression tag	UNP P49770
D	-5	GLU	-	expression tag	UNP P49770
D	-4	ASN	-	expression tag	UNP P49770
D	-3	LEU	-	expression tag	UNP P49770
D	-2	TYR	-	expression tag	UNP P49770
D	-1	PHE	-	expression tag	UNP P49770
D	0	GLN	-	expression tag	UNP P49770
D	1	SER	-	expression tag	UNP P49770

- Molecule 3 is a protein called Translation initiation factor eIF-2B subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	351	Total	C	N	O	S	0	0
			2734	1730	487	503	14		
3	F	346	Total	C	N	O	S	0	0
			2693	1704	478	497	14		

- Molecule 4 is a protein called Translation initiation factor eIF-2B subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	265	Total	C	N	O	S	0	0
			1977	1275	330	361	11		
4	H	266	Total	C	N	O	S	0	0
			1966	1268	328	360	10		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-16	MET	-	initiating methionine	UNP Q14232
G	-15	HIS	-	expression tag	UNP Q14232
G	-14	HIS	-	expression tag	UNP Q14232
G	-13	HIS	-	expression tag	UNP Q14232
G	-12	HIS	-	expression tag	UNP Q14232
G	-11	HIS	-	expression tag	UNP Q14232
G	-10	HIS	-	expression tag	UNP Q14232
G	-9	GLY	-	expression tag	UNP Q14232
G	-8	GLY	-	expression tag	UNP Q14232
G	-7	GLY	-	expression tag	UNP Q14232
G	-6	SER	-	expression tag	UNP Q14232
G	-5	GLU	-	expression tag	UNP Q14232
G	-4	ASN	-	expression tag	UNP Q14232
G	-3	LEU	-	expression tag	UNP Q14232
G	-2	TYR	-	expression tag	UNP Q14232
G	-1	PHE	-	expression tag	UNP Q14232
G	0	GLN	-	expression tag	UNP Q14232
G	1	SER	-	expression tag	UNP Q14232
H	-16	MET	-	initiating methionine	UNP Q14232
H	-15	HIS	-	expression tag	UNP Q14232
H	-14	HIS	-	expression tag	UNP Q14232
H	-13	HIS	-	expression tag	UNP Q14232
H	-12	HIS	-	expression tag	UNP Q14232
H	-11	HIS	-	expression tag	UNP Q14232
H	-10	HIS	-	expression tag	UNP Q14232
H	-9	GLY	-	expression tag	UNP Q14232
H	-8	GLY	-	expression tag	UNP Q14232
H	-7	GLY	-	expression tag	UNP Q14232
H	-6	SER	-	expression tag	UNP Q14232
H	-5	GLU	-	expression tag	UNP Q14232
H	-4	ASN	-	expression tag	UNP Q14232
H	-3	LEU	-	expression tag	UNP Q14232
H	-2	TYR	-	expression tag	UNP Q14232
H	-1	PHE	-	expression tag	UNP Q14232
H	0	GLN	-	expression tag	UNP Q14232
H	1	SER	-	expression tag	UNP Q14232

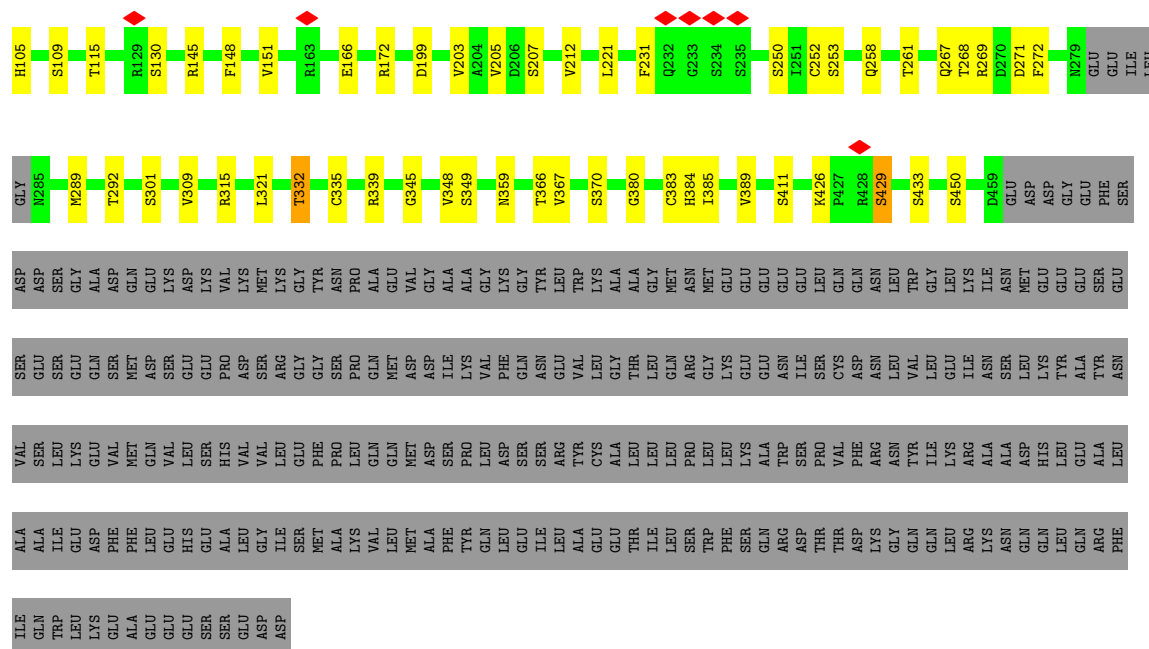
- Molecule 5 is a protein called Translation initiation factor eIF-2B subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	215	Total	C	N	O	S	0	0
			1682	1094	284	291	13		

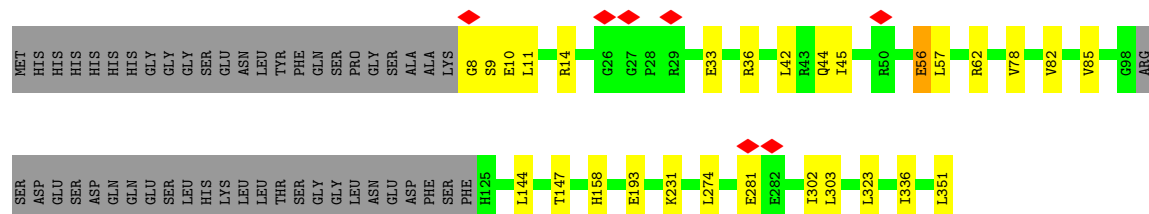
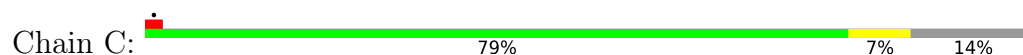
Continued on next page...

Continued from previous page...

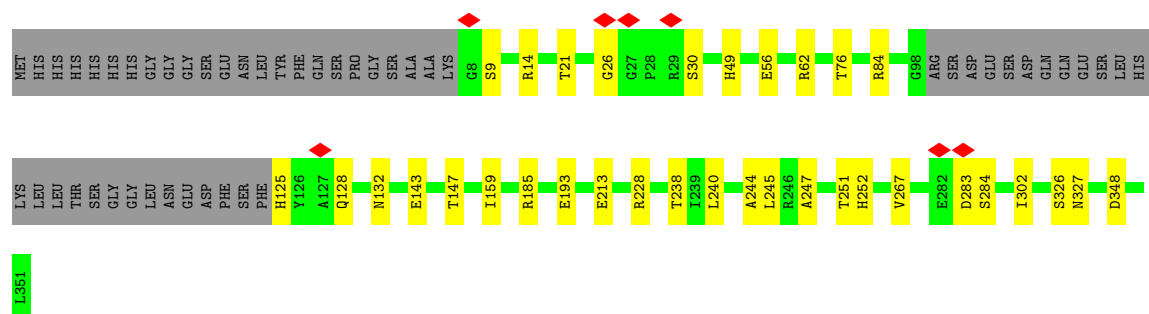
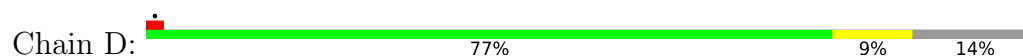
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	J	229	1794	1164	303	312	15	0	0



- Molecule 2: Translation initiation factor eIF-2B subunit beta



- Molecule 2: Translation initiation factor eIF-2B subunit beta

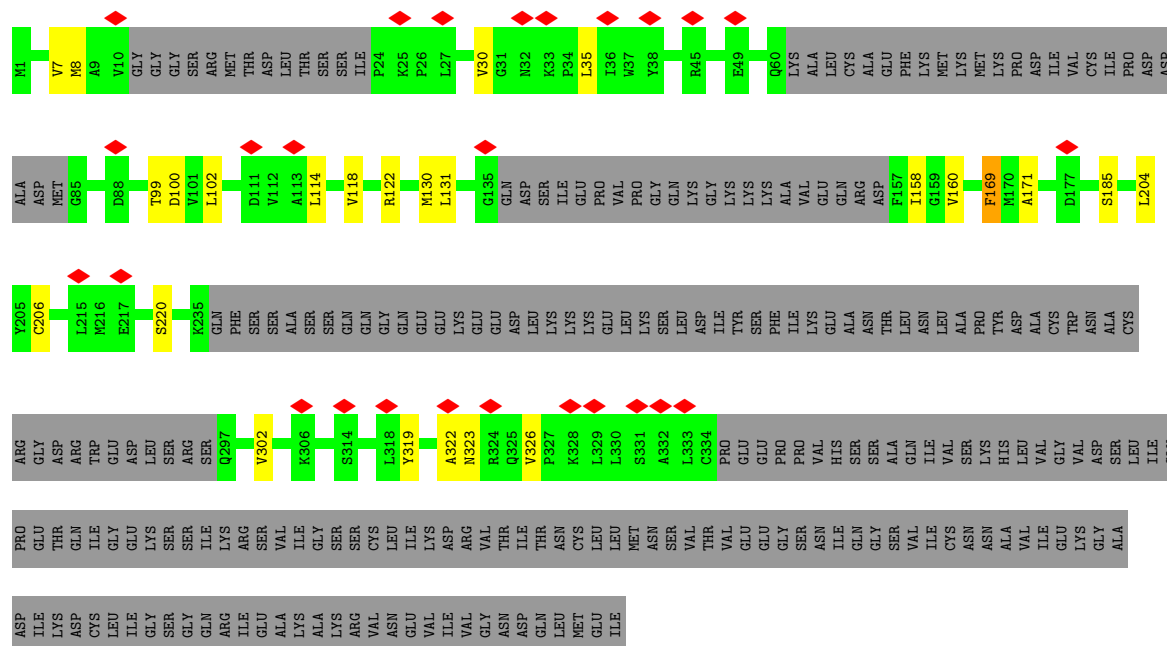
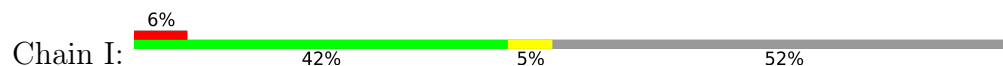


- Molecule 3: Translation initiation factor eIF-2B subunit delta

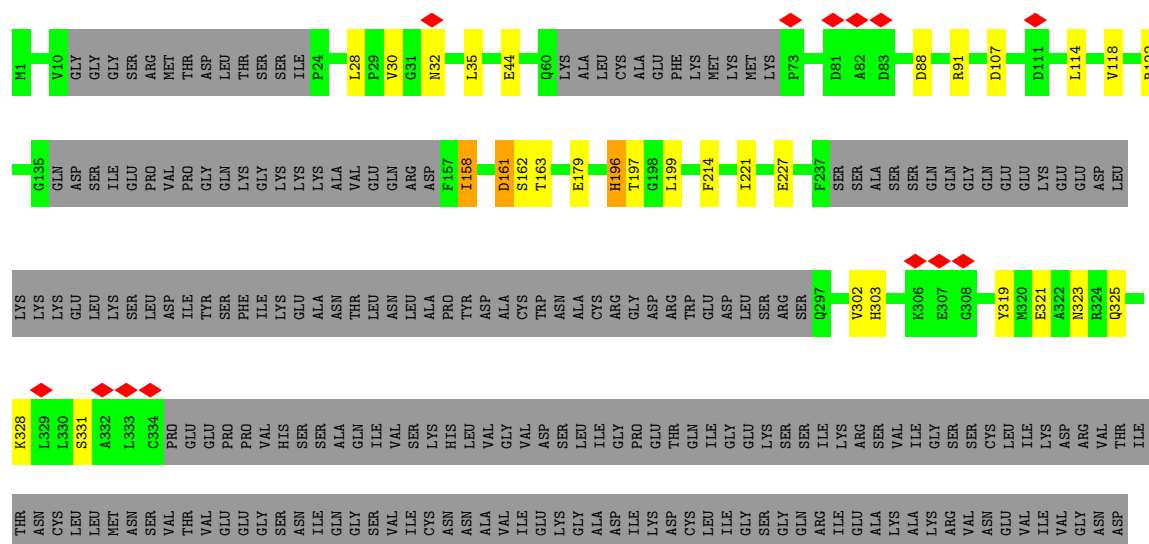




- Molecule 5: Translation initiation factor eIF-2B subunit gamma



- Molecule 5: Translation initiation factor eIF-2B subunit gamma



GLN
LEU
MET
GLU
ILE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	461805	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	67	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.693	Depositor
Minimum map value	-1.422	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.5	Depositor
Map size (\AA)	334.0, 334.0, 334.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.835, 0.835, 0.835	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/3262	0.48	1/4446 (0.0%)
1	B	0.25	0/3262	0.48	1/4446 (0.0%)
2	C	0.24	0/2526	0.40	0/3417
2	D	0.24	0/2519	0.40	0/3408
3	E	0.24	0/2786	0.39	0/3787
3	F	0.24	0/2744	0.40	0/3730
4	G	0.33	0/2009	0.52	2/2721 (0.1%)
4	H	0.33	0/1997	0.44	0/2711
5	I	0.24	0/1708	0.40	0/2304
5	J	0.24	0/1823	0.42	0/2461
All	All	0.26	0/24636	0.44	4/33431 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	49	LEU	CB-CG-CD2	6.36	121.82	111.00
1	A	104	GLU	CA-CB-CG	6.03	126.66	113.40
1	B	104	GLU	CA-CB-CG	6.02	126.64	113.40
4	G	49	LEU	CB-CG-CD1	6.01	121.21	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	57	PHE	Peptide
1	B	57	PHE	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3195	0	3142	29	0
1	B	3195	0	3142	31	0
2	C	2479	0	2494	19	0
2	D	2472	0	2486	17	0
3	E	2734	0	2794	17	0
3	F	2693	0	2745	17	0
4	G	1977	0	1986	46	0
4	H	1966	0	1955	31	0
5	I	1682	0	1748	14	0
5	J	1794	0	1856	18	0
All	All	24187	0	24348	225	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 225 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:49:LEU:HD11	4:H:72:PHE:HE2	1.23	1.04
4:H:49:LEU:CD1	4:H:72:PHE:HE2	1.74	0.98
4:G:48:ASN:O	4:G:51:SER:OG	1.82	0.95
4:G:14:MET:HE2	4:G:28:ARG:HB2	1.48	0.93
4:H:46:ARG:HH11	4:H:46:ARG:HB2	1.34	0.92

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	410/721 (57%)	390 (95%)	19 (5%)	1 (0%)	47	78
1	B	410/721 (57%)	390 (95%)	19 (5%)	1 (0%)	47	78
2	C	314/368 (85%)	303 (96%)	11 (4%)	0	100	100
2	D	314/368 (85%)	302 (96%)	12 (4%)	0	100	100
3	E	349/523 (67%)	345 (99%)	4 (1%)	0	100	100
3	F	344/523 (66%)	342 (99%)	2 (1%)	0	100	100
4	G	257/322 (80%)	250 (97%)	7 (3%)	0	100	100
4	H	258/322 (80%)	252 (98%)	6 (2%)	0	100	100
5	I	205/452 (45%)	189 (92%)	16 (8%)	0	100	100
5	J	219/452 (48%)	201 (92%)	18 (8%)	0	100	100
All	All	3080/4772 (64%)	2964 (96%)	114 (4%)	2 (0%)	54	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	PRO
1	B	58	PRO

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	351/626 (56%)	328 (93%)	23 (7%)	16	44

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	351/626 (56%)	328 (93%)	23 (7%)	16	44
2	C	268/312 (86%)	266 (99%)	2 (1%)	84	95
2	D	266/312 (85%)	259 (97%)	7 (3%)	46	79
3	E	307/444 (69%)	304 (99%)	3 (1%)	76	93
3	F	302/444 (68%)	301 (100%)	1 (0%)	92	98
4	G	206/274 (75%)	193 (94%)	13 (6%)	18	46
4	H	201/274 (73%)	193 (96%)	8 (4%)	31	65
5	I	182/398 (46%)	178 (98%)	4 (2%)	52	83
5	J	196/398 (49%)	190 (97%)	6 (3%)	40	74
All	All	2630/4108 (64%)	2540 (97%)	90 (3%)	40	71

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	492	THR
4	G	273	VAL
4	G	9	TYR
4	G	45	LEU
4	H	49	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	464	GLN
4	G	243	GLN
4	G	222	GLN
4	H	48	ASN
3	E	213	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

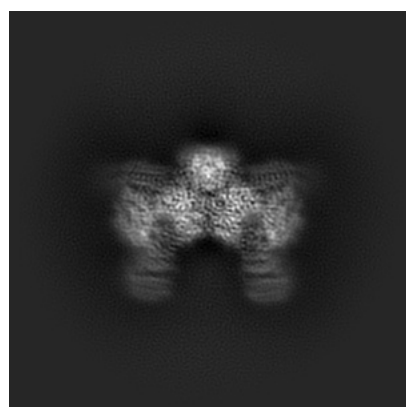
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23209. These allow visual inspection of the internal detail of the map and identification of artifacts.

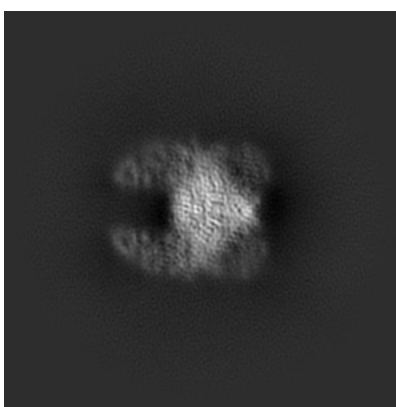
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

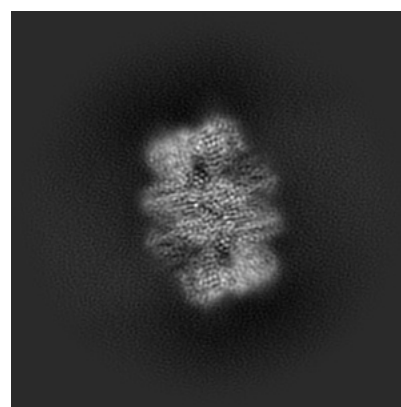
6.1.1 Primary map



X



Y

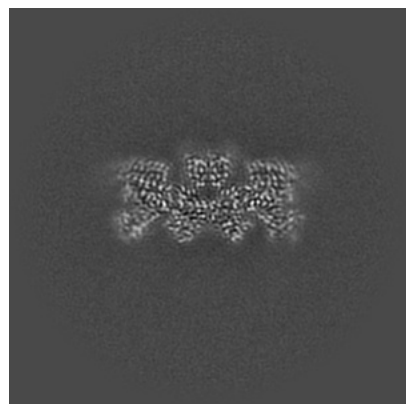


Z

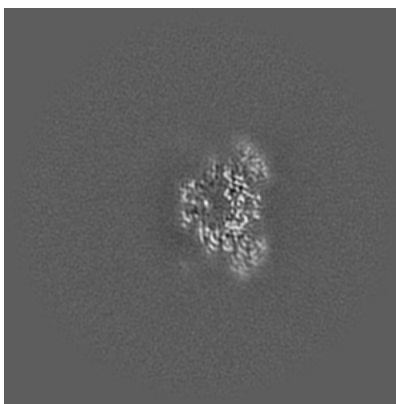
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

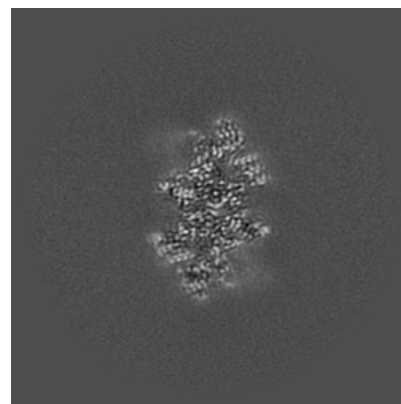
6.2.1 Primary map



X Index: 200



Y Index: 200

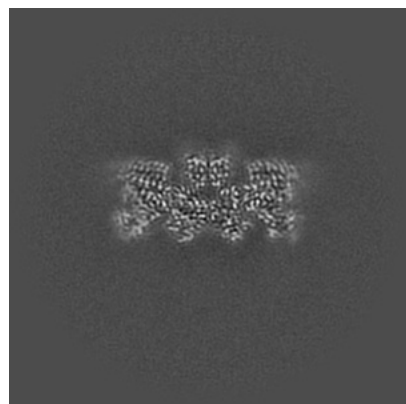


Z Index: 200

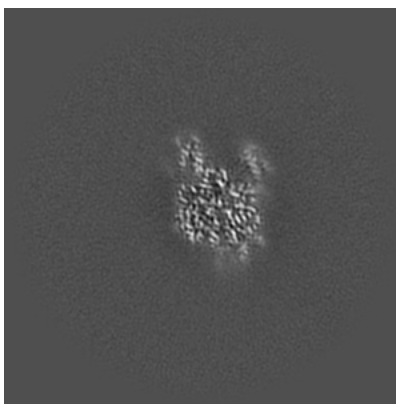
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

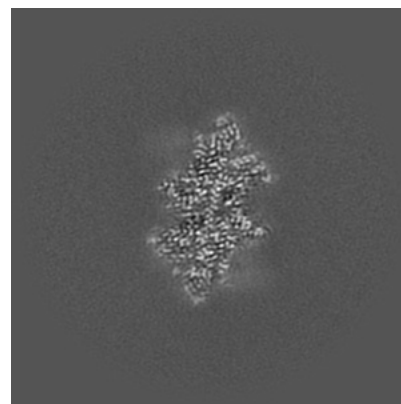
6.3.1 Primary map



X Index: 199



Y Index: 186



Z Index: 203

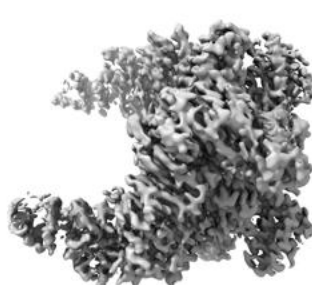
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

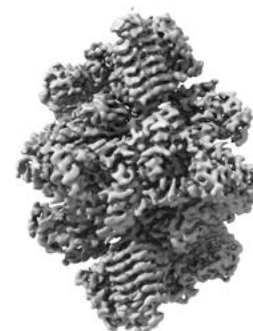
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

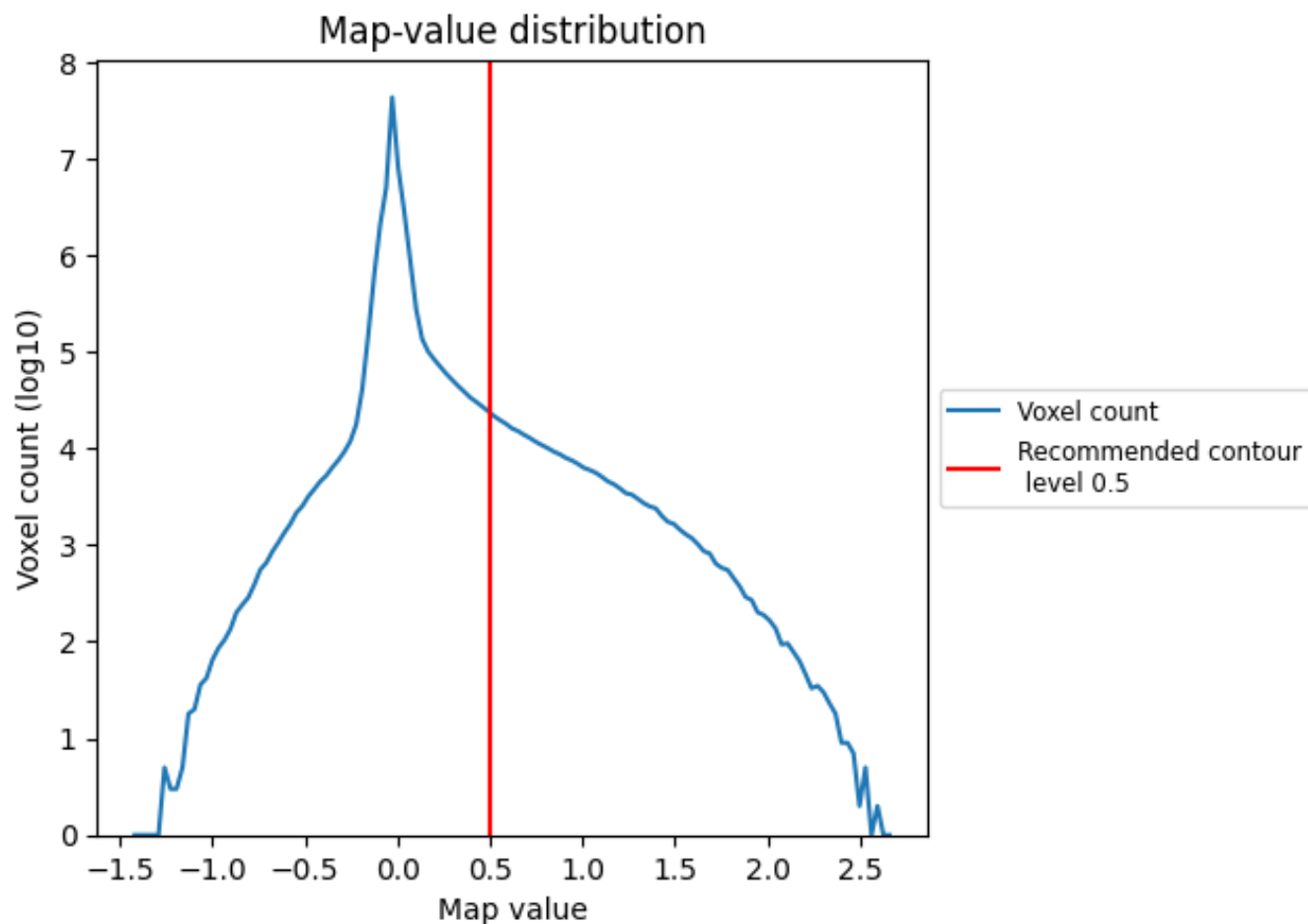
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

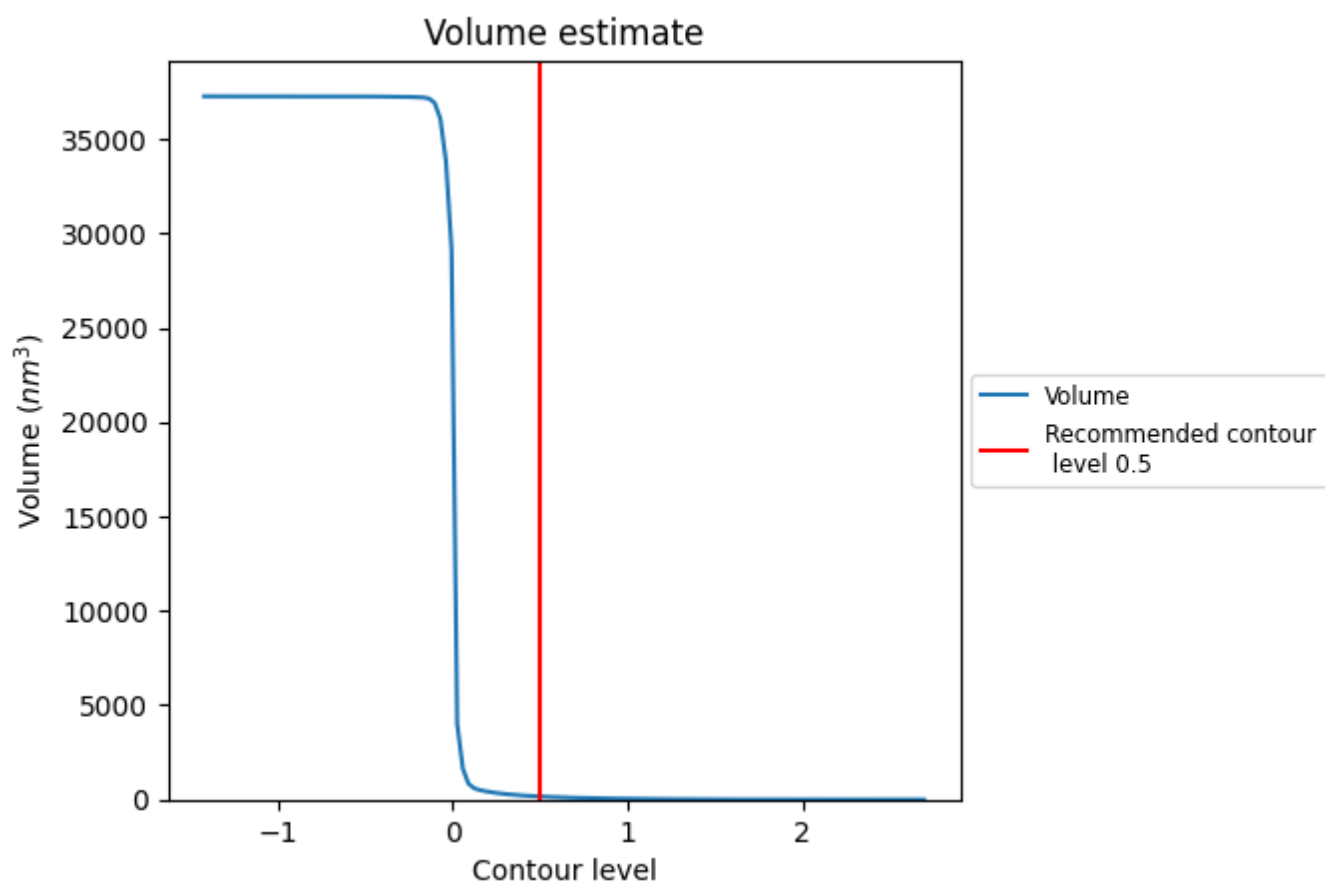
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

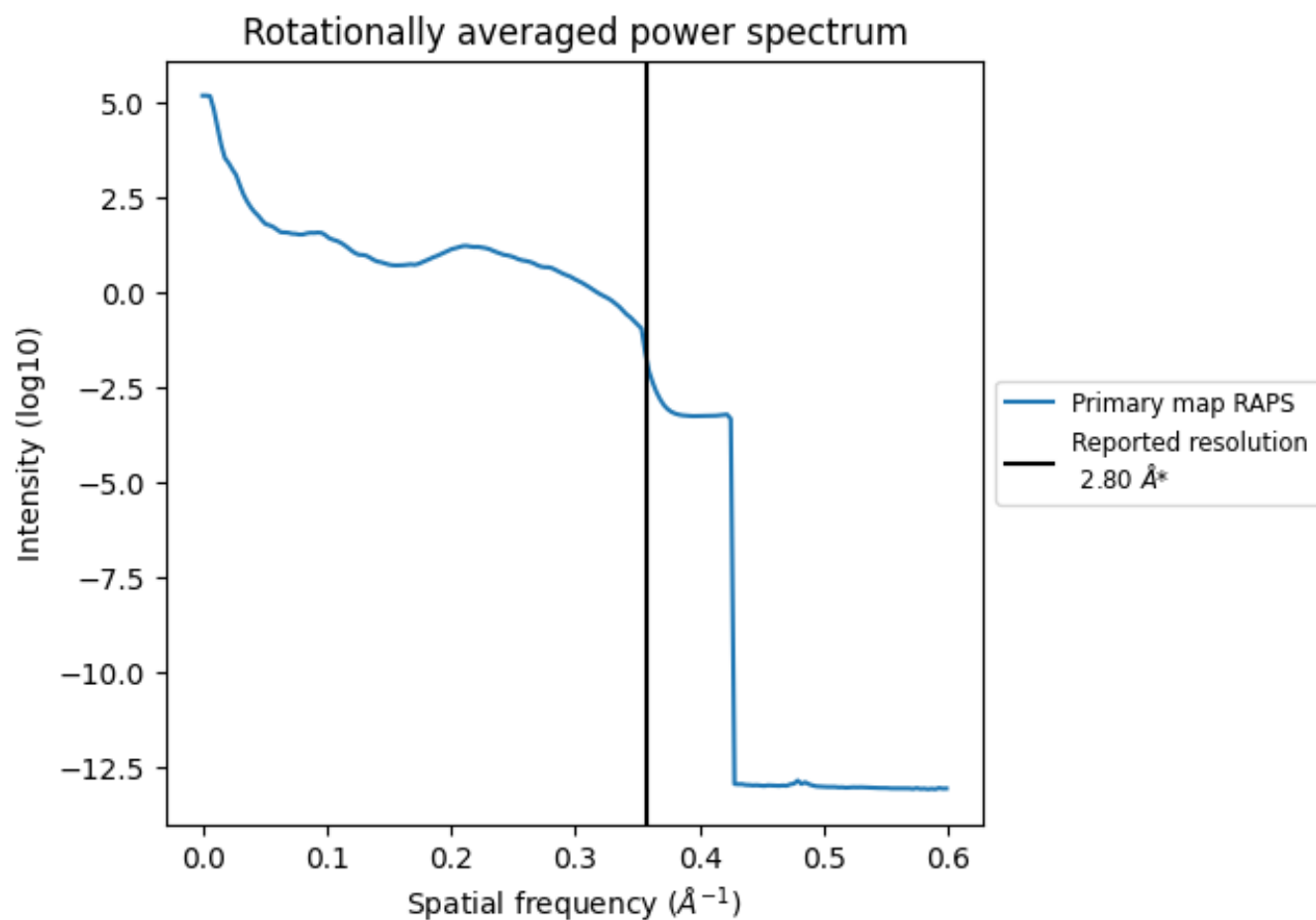
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 161 nm³; this corresponds to an approximate mass of 145 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

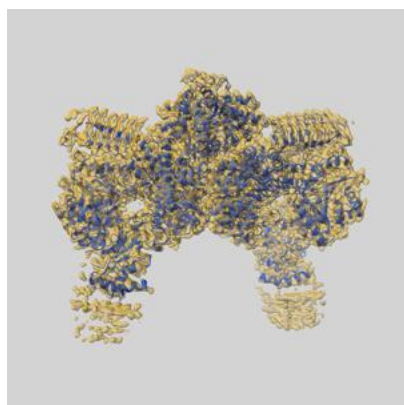
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

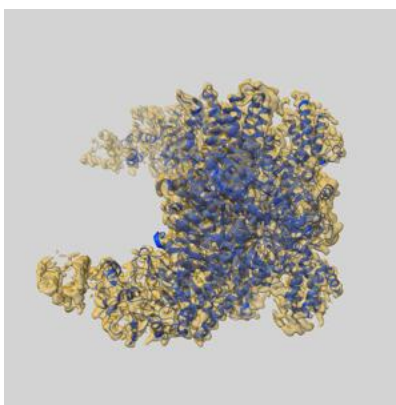
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23209 and PDB model 7L70. Per-residue inclusion information can be found in section 3 on page 8.

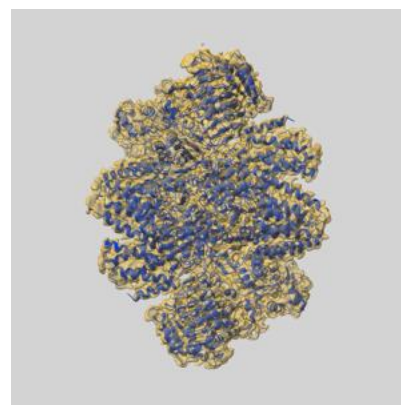
9.1 Map-model overlay [i](#)



X



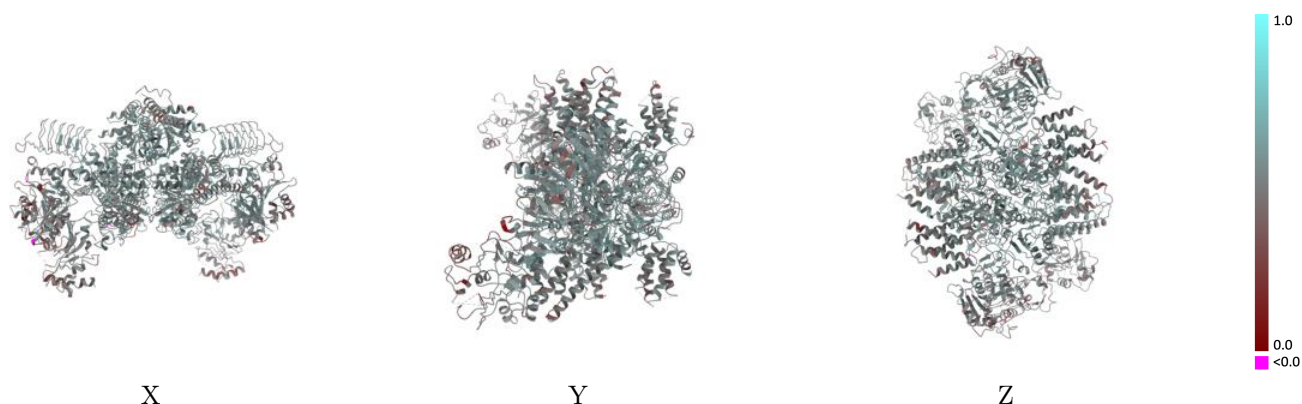
Y



Z

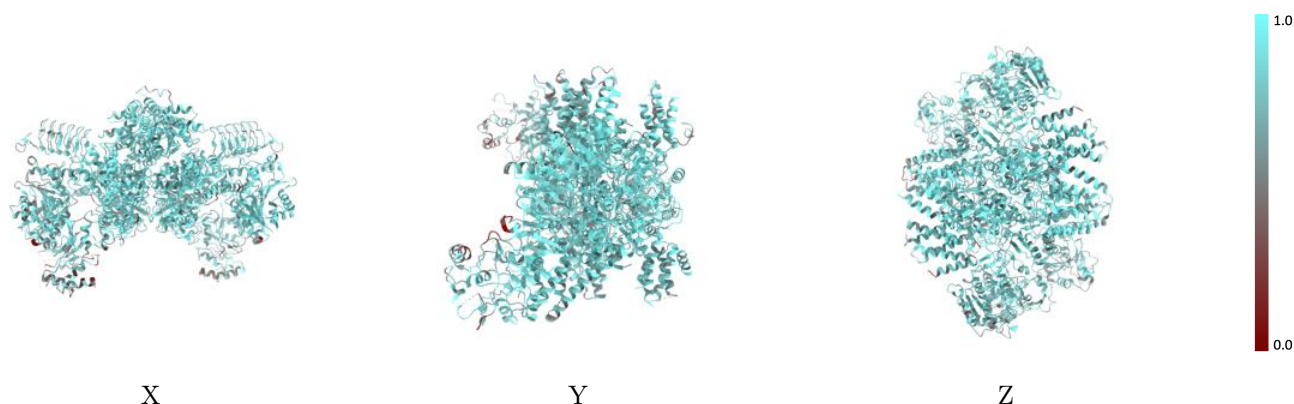
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



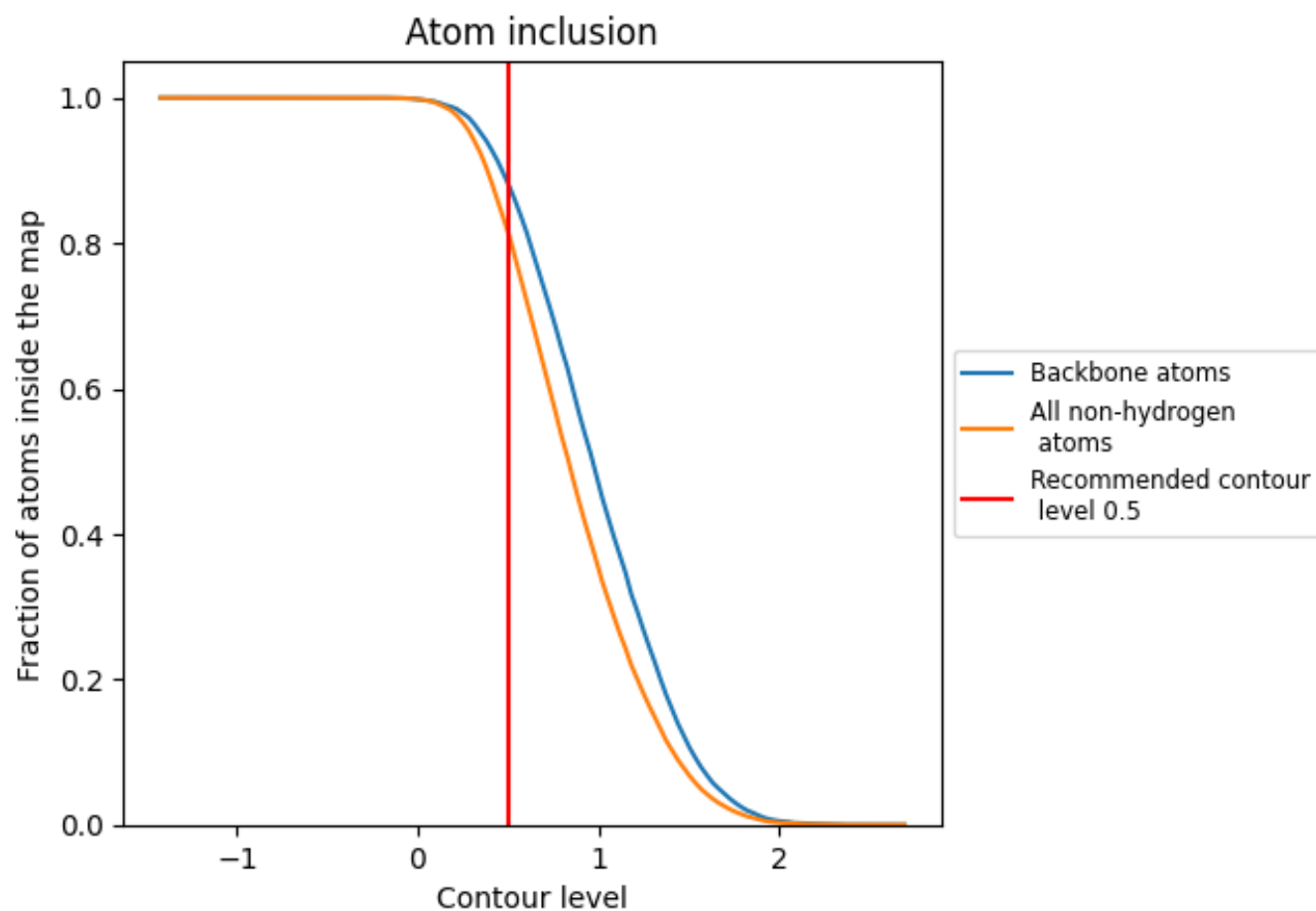
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8150	<div><div></div></div> 0.5090
A	<div><div></div></div> 0.7517	<div><div></div></div> 0.4730
B	<div><div></div></div> 0.8169	<div><div></div></div> 0.5080
C	<div><div></div></div> 0.8442	<div><div></div></div> 0.5210
D	<div><div></div></div> 0.8470	<div><div></div></div> 0.5130
E	<div><div></div></div> 0.8559	<div><div></div></div> 0.5360
F	<div><div></div></div> 0.8484	<div><div></div></div> 0.5300
G	<div><div></div></div> 0.8463	<div><div></div></div> 0.5330
H	<div><div></div></div> 0.8490	<div><div></div></div> 0.5280
I	<div><div></div></div> 0.6990	<div><div></div></div> 0.4630
J	<div><div></div></div> 0.7639	<div><div></div></div> 0.4820

1.0

0.0

<0.0